

05/90
7/206

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#3



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,564

DATE: 02/24/2003

TIME: 10:15:32

Input Set : N:\Crf3\RULE60\09770564.raw.txt

Output Set: N:\CRF4\02242003\I770564.raw

4 <110> APPLICANT: Crasta, Oswald R.
5 Duvick, Jonathan P.
6 Folkerts, Otto
7 Gilliam, Jacob T.
8 Maddox, Joyce R.
11 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
12 Polynucleotides and Related Polypeptides and Methods of Use
15 <130> FILE REFERENCE: 0875
17 <140> CURRENT APPLICATION NUMBER: US 09/770,564
18 <141> CURRENT FILING DATE: 2001-01-26
20 <150> PRIOR APPLICATION NUMBER: US 09/352,168
21 <151> PRIOR FILING DATE: 1999-07-12
23 <150> PRIOR APPLICATION NUMBER: 60/092,936
24 <151> PRIOR FILING DATE: 1998-07-25
26 <160> NUMBER OF SEQ ID NOS: 33
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 372
32 <212> TYPE: DNA
33 <213> ORGANISM: Exophiala spinifera.
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (346)...(346)
38 <223> OTHER INFORMATION: n = A,T,C or G
40 <400> SEQUENCE: 1
41 gggccccggc gttctcgtag gctgcgcgga gttggtccca gacagacttt tgtcgtaccc 60
42 gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc 120
43 attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt 180
44 ggaggacgcc cgagaaggcct tggcgcgcc accacggctt gtcccatacg aagactatct 240
45 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgcc ggaagagggt 300
W--> 46 gtgaaaatgt caaggtggga tacaagggttg tcggtaacga aaccancacc ttttgcttc 360
47 ggaacacggc gc 372
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 182
51 <212> TYPE: DNA
52 <213> ORGANISM: Exophiala spinifera.
54 <400> SEQUENCE: 2
55 gaatttccg ccaatgcttg cttctcgccg ggaagagggtg gtgaaaatgt caaggtggga 60
56 tacaagggttg tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccggggcc 120
57 gatcgactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180
58 ac 182
60 <210> SEQ ID NO: 3
61 <211> LENGTH: 29

RAW SEQUENCE LISTING

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 Output Set: N:\CRF4\02242003\I770564.raw

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62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
68 <400> SEQUENCE: 3
69 tggtttcgtt accgacaacc ttgtatccc                                29
71 <210> SEQ ID NO: 4
72 <211> LENGTH: 28
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Desiged oligonucleotide for 5' RACE, N21968
79 <400> SEQUENCE: 4
80 gagtttgtcc cagacagact tttgtcgt                                28
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 1389
84 <212> TYPE: DNA
85 <213> ORGANISM: Exophiala spinifera
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)...(1386)
91 <400> SEQUENCE: 5
92 gac aac gtt gcg gac gtg gta gtg gtc ggc gct ggc ttg agc ggt ttg      48
93 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
94   1           5           10          15
96 gag acg gca cgc aaa gtc cag gcc gtc ggt ctg tcc tgc ctc gtt ctt      96
97 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
98   20          25          30
100 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt     144
101 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
102    35          40          45
104 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac     192
105 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
106    50          55          60
108 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag     240
109 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
110    65          70          75          80
112 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac     288
113 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
114    85          90          95
116 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag     336
117 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
118    100         105         110
120 gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc     384
121 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
122    115         120         125
124 gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg     432
125 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
126    130         135         140

```

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Input Set : N:\CrF3\RULE60\09770564.raw.txt
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128	ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
129	Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
130	145 150 155 160	
132	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
133	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
134	165 170 175	
136	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
137	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
138	180 185 190	
140	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
141	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
142	195 200 205	
144	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
145	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
146	210 215 220	
148	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
149	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
150	225 230 235 240	
152	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768
153	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
154	245 250 255	
156	gcc gtg ttc cga agc aaa aag gtg gtt tcg tta ccg aca acc ttg	816
157	Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu	
158	260 265 270	
160	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
161	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
162	275 280 285	
164	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
165	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
166	290 295 300	
168	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
169	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
170	305 310 315 320	
172	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
173	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
174	325 330 335	
176	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
177	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
178	340 345 350	
180	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
181	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
182	355 360 365	
184	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
185	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
186	370 375 380	
188	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
189	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
190	385 390 395 400	
192	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248

RAW SEQUENCE LISTING

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Output Set: N:\CRF4\02242003\I770564.raw

193 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 194 405 410 415
 196 gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg 1296
 197 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 198 420 425 430
 200 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa 1344
 201 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 202 435 440 445
 204 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 1386
 205 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 206 450 455 460
 208 tag 1389
 210 <210> SEQ ID NO: 6
 211 <211> LENGTH: 462
 212 <212> TYPE: PRT
 213 <213> ORGANISM: Exophiala spinifera
 215 <400> SEQUENCE: 6
 216 Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu
 217 1 5 10 15
 218 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 219 20 25 30
 220 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 221 35 40 45
 222 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 223 50 55 60
 224 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 225 65 70 75 80
 226 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 227 85 90 95
 228 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 229 100 105 110
 230 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 231 115 120 125
 232 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 233 130 135 140
 234 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 235 145 150 155 160
 236 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 237 165 170 175
 238 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 239 180 185 190
 240 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 241 195 200 205
 242 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 243 210 215 220
 244 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 245 225 230 235 240
 246 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 247 245 250 255

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```

248 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
249      260          265          270
250 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
251      275          280          285
252 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
253      290          295          300
254 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
255      305          310          315          320
256 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
257      325          330          335
258 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
259      340          345          350
260 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
261      355          360          365
262 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
263      370          375          380
264 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
265      385          390          395          400
266 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
267      405          410          415
268 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
269      420          425          430
270 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
271      435          440          445
272 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
273      450          455          460

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275 <210> SEQ ID NO: 7

276 <211> LENGTH: 1442

277 <212> TYPE: DNA

278 <213> ORGANISM: Exophiala spinifera

280 <220> FEATURE:

281 <221> NAME/KEY: CDS

282 <222> LOCATION: (1)...(646)

284 <221> NAME/KEY: intron

285 <222> LOCATION: (647)...(699)

W--> 287 <221> CDS

288 <222> LOCATION: (700)...(1439)

W--> 290 <400> 7

```

291 gac aac gtt gcg gac gtg gta gtg ggc gct ggc ttg agc ggt ttg      48
292 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
293 1           5           10          15
295 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
296 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
297 20          25          30
299 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
300 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
301 35          40          45
303 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
304 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/24/2003
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Input Set : N:\Crf3\RULE60\09770564.raw.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 346

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:18,20,24,25,26,27,28,29,30,31,32,33

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09770564.raw.txt
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L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300
 L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
 L:290 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
 L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
 L:802 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
 L:1044 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
 L:1048 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
 L:1052 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
 L:1343 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
 L:1350 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:1351 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:1353 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
 L:1357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
 L:1816 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:1820 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
 L:1824 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
 L:1828 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
 L:1832 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
 L:1835 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
 L:1839 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
 L:2102 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
 ORGANISM:Unknown

L:2102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:2102
 L:2240 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:2244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
 L:2248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
 L:2252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
 L:2256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
 L:2259 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
 L:2263 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
 L:2523 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
 ORGANISM:Unknown

L:2523 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2523
 L:2660 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:2663 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
 L:2667 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
 L:2671 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
 L:2675 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
 L:2679 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
 L:2683 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
 L:2994 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
 ORGANISM:Unknown

L:2994 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
 ORGANISM:Unknown
 L:2994 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2994
 L:3158 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:3159 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:3161 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:3165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
 L:3169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
 L:3173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
 L:3177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09770564.raw.txt
Output Set: N:\CRF4\02242003\I770564.raw

L:3180 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3491 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Unknown
L:3491 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Unknown
L:3491 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:3491
L:3654 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3657 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3661 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3665 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3669 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3673 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:3888 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:Unknown